Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (Currently Amended) A method for preparing at least one complementary copy of specified sequences of support-bound singled-stranded nucleic acids, comprising the steps:

(a) providing a support with a surface which comprises a plurality of positions at each of which different nucleic acid fragments are present, comprising base sequences which are chosen to be complementary to the specified sequences of nucleic acids to be prepared,

(b) adding nucleotide building blocks and an enzyme which brings about generation of complementary copies of the base sequences from (a),

(c) generating at least one singled-stranded complementary copy of the nucleic acids to be prepared in (a), and

(d) detaching the singled-stranded nucleic acids generated in step (c) and, where appropriate, providing for further operations.

2. (Currently Amended) A method for preparing a predetermined nucleic acid double strand having its sequence specified by a user, comprising the steps:

(a) providing a support with a surface which comprises a plurality of positions at each of which different nucleic acid fragments are present, comprising base sequences which

are chosen to be complementary to partial sequences of the nucleic acid double strand having a user-specified sequence to be prepared,

(b) adding nucleotide building blocks and an enzyme which brings about generation of complementary copies of the base sequences from (a),

(c) generating single-stranded complementary copies of the nucleic acids to be prepared in (a), and

(d) assembling the singled-stranded partial sequences generated in step (c) to give the desired nucleic acid double strand.

3. (Previously Presented) The method as claimed in claim 1, characterized in that the support is selected from flat supports, porous supports, reaction supports with electrodes, reaction supports with particles or beads, microfluidic reaction supports which optionally have surface modifications such as gels, linkers, spacers, polymers, amorphous layers or/and 3D matrices, and combinations of the aforementioned supports.

4. (Previously Presented) The method as claimed in claim 1, characterized in that a microfluidic support is provided.

5. (Previously Presented) The method as claimed in claim 1, characterized in that the nucleic acid fragments from (a) are generated by spatially resolved in situ synthesis on the support.

6. (Original) The method as claimed in claim 5, characterized in that the nucleic acid fragments from (a) are synthesized by spatially or/and time-resolved illumination by means of a programmable light source matrix.

7. (Original) The method as claimed in claim 6, characterized in that the spatially or/and time-resolved synthesis takes place in a microfluidic support with one or more fluidic reaction chambers and one or more reaction zones within a fluidic reaction chamber.

8. (Previously Presented) The method as claimed in claim 2, characterized in that the assembly of the partial sequences in step (c) takes place at least partly in one or more steps on the support.

9. (Previously Presented) The method as claimed in claim 1, the nucleic acid fragments from (a) are chosen so that the nucleic acids or partial sequences formed in step (c) can be joined to give nucleic acid double-stranded hybrids.

10. (Previously Presented) The method as claimed in claim 2, wherein a plurality of nucleic acids or partial sequences which form a strand of the nucleic acid double strand are covalently connected together.

11. (Original) The method as claimed in claim 10, characterized in that the covalent connection comprises a treatment with ligase or/and a filling-in of gaps in the strands

with DNA polymerase.

12. (Previously Presented) The method as claimed in claim 1, characterized in that step (b) comprises the addition of at least one primer for each position of the support, the primer being complementary to part of the nucleic acid fragment located at this position and step (b) comprising an elongation of the primer.

13. (Previously Presented) The method as claimed in claim 1, characterized in that double-stranded nucleic acid fragments are provided in step (a), with at least one strand being tethered to the surface of the support.

14. (Original) The method as claimed in claim 13, characterized in that step (b) comprises transcription of double-stranded DNA fragments or/and replication of double-stranded RNA fragments.

15. (Previously Presented) The method as claimed in claim 1, characterized in that nucleic acid fragments comprising a self-priming 3' end are provided in step (a), and step (b) comprises elongation of the 3' end.

16. (Original) The method as claimed in claim 15, which comprises elimination of the elongation product.

17. (Previously Presented) The method as claimed in claim 1, characterized in that

double-stranded, circular nucleic acid fragments are provided in step (a), one strand being tethered to the surface of the support, and the other strand comprising a self-priming 3' end, and step (b) comprising elongation of the 3' end.

18. (Original) The method as claimed in claim 17, which comprises elimination of the elongation product.

19. (Previously Presented) The method as claimed in claim 1, characterized in that the nucleic acid fragments from (a) are generated by: provision of capture probes at the positions and binding of nucleic acid fragments from a fluid passed over the support to the capture probes, where the capture probes are complementary to partial regions of the nucleic acid fragments.

20. (Previously Presented) The method as claimed in claim 1, wherein recognition sequences for specific interaction with molecules such as proteins, nucleic acids, peptides, drugs, saccharides, lipids, hormones or/and organic compounds are present at one or more positions in the sequence of the generated nucleic acids.

21. (Previously Presented) The method as claimed in claim 1, wherein the sequence of the generated nucleic acids is a naturally occurring sequence, a non-naturally occurring sequence or a combination thereof.

22. (Previously Presented) The method as claimed in claim 1, characterized in that the

sequence is taken from a database, from a sequencing experiment or from an apparatus for integrated synthesis and analysis of polymers.

23. (Previously Presented) The method as claimed in claim 1, characterized in that the nucleotide building blocks may comprise naturally occurring nucleotides, modified nucleotides or mixtures thereof.

24. (Previously Presented) The method as claimed in claim 1, characterized in that modified nucleotide building blocks are used for labeling and subsequent detection of the nucleic acids or of the joined nucleic acid double strands.

25. (Original) The method as claimed in claim 24, characterized in that molecules to be detected in a light-dependent or/and electrochemical manner are used as labeling groups.

26. (Previously Presented) The method of claim 1, wherein said prepared nucleic acids are tools for therapeutic or pharmacological purposes.

27. (Previously Presented) The method of claim 1, wherein said prepared nucleic acids are tools for diagnostic purposes.

28. (Previously Presented) The method of claim 26, further comprising transferring said prepared nucleic acids into effector cells.

29. (Previously Presented) The method of claim 1, wherein said prepared nucleic acids are stabilized, condensed or/and topologically manipulated during a stepwise combination and joining or subsequent thereto.

30. (Previously Presented) The method of claim 29 wherein said stabilization, condensation or/and topological manipulation is effected by functional molecules such as histones or topoisomerases.

31. (Previously Presented) The method of claim 1, wherein said prepared nucleic acids are propagatable cloning vectors.

32. (Previously Presented) The method as claimed in claim 2, wherein recognition sequences for specific interaction with molecules selected from the group consisting of proteins, nucleic acids, peptides, drugs, saccharides, lipids, hormones, and organic compounds are present at one or more positions in the sequence of the generated nucleic acid double strand.

33. (Previously Presented) The method as claimed in claim 2, wherein the sequence of the generated nucleic acid double strand is a naturally occurring sequence, a non-naturally occurring sequence, or a combination thereof.